

A' *new*  
p. 604 and pp. 688-692. The ability of a segment to serve as a membrane anchor can be demonstrated by observing whether a polypeptide having such a segment co-purifies with a membrane fraction. Alternatively, a segment can be a membrane-anchor if, after fusing it to the second and third segments, it is shown that the polypeptide possesses elongase KCS activity in an *in vitro* yeast microsome assay, since elongase KCS polypeptides are active when anchored to a membrane. As another alternative, computer algorithms, such as Predict Protein or META Predict Protein, can be used to predict the presence of a transmembrane domain within a segment, and hence, the ability of that polypeptide segment to serve as a membrane anchor.

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Please replace the paragraph on page 10, lines 18-28 with the following amended paragraph:

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A' *new*  
A percent identity for any subject nucleic acid or amino acid sequence (*e.g.*, any of the fatty acid elongase chimeras described herein) relative to another "target" nucleic acid or amino acid sequence can be determined as follows. First, a target nucleic acid or amino acid sequence of the invention can be compared and aligned to a subject nucleic acid or amino acid sequence, preferably using the BLAST 2 Sequences (BI2seq) program from the stand-alone version of BLASTZ containing BLASTN and BLASTP (*e.g.*, version 2.0.14). The stand-alone version of BLASTZ can be obtained at Fish & Richardson's website or the National Center for Biotechnology Information (NCBI) website. Instructions explaining how to use BLASTZ, and specifically the BI2seq program, can be found in the 'readme' file accompanying BLASTZ. The programs also are described in detail by Karlin et al. (*Proc. Natl. Acad. Sci. USA*, 87:2264 (1990) and 90:5873 (1993)) and Altschul et al. (*Nucl. Acids Res.*, 25:3389 (1997)).

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In the Claims:

Please cancel claims 1-11, 14, 17, 22, and 25 without prejudice. Please replace claims 12, 13, 15, 16, 20, and 21 with the following amended claims 12, 13, 15, 16, 20, and 21. For convenience, a complete set of pending claims is shown below.

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A' *new*  
--12. (Amended) An isolated nucleic acid encoding a polypeptide, said polypeptide comprising in the amino-terminal to carboxy-terminal direction: